

1645 #8
JWS
11/30/02

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/735,786A

DATE: 11/21/2002

TIME: 11:07:19

RECEIVED

NOV 27 2002

TECH CENTER 1600/2900

Input Set : A:\13407-016002.txt

Output Set: N:\CRF4\11212002\I735786A.raw

4 <110> APPLICANT: Guarente, Leonard
 5 Imai, Shin-ichiro
 6 Armstrong, Christopher
 7 Tissenbaum, Heidi A.
 9 <120> TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH ALTER HISTONE
 10 PROTEIN ACETYLATION, DECREASE AGING, INCREASE LIFESPAN
 12 <130> FILE REFERENCE: 13407-016002
 14 <140> CURRENT APPLICATION NUMBER: US 09/735,786A
 15 <141> CURRENT FILING DATE: 2000-12-13
 17 <150> PRIOR APPLICATION NUMBER: US 09/461,580
 18 <151> PRIOR FILING DATE: 1999-12-15
 20 <160> NUMBER OF SEQ ID NOS: 38
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 737
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Mus musculus
 29 <400> SEQUENCE: 1
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 31 1 5 10 15
 32 Ala Ala Ala Ala Met Glu Ala Ala Ser Gln Pro Ala Asp Glu Pro Leu
 33 20 25 30
 34 Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Gly Arg Ser Pro Gly
 35 35 40 45
 36 Glu Pro Ser Ala Ala Val Ala Pro Ala Ala Ala Gly Cys Glu Ala Ala
 37 50 55 60
 38 Ser Ala Ala Ala Pro Ala Ala Leu Trp Arg Glu Ala Ala Gly Ala Ala
 39 65 70 75 80
 40 Ala Ser Ala Glu Arg Glu Ala Pro Ala Thr Ala Val Ala Gly Asp Gly
 41 85 90 95
 42 Asp Asn Gly Ser Gly Leu Arg Arg Glu Pro Arg Ala Ala Asp Asp Phe
 43 100 105 110
 44 Asp Asp Asp Glu Gly Glu Glu Glu Asp Glu Ala Ala Ala Ala Ala
 45 115 120 125
 46 Ala Ala Ala Ile Gly Tyr Arg Asp Asn Leu Leu Leu Thr Asp Gly Leu
 47 130 135 140
 48 Leu Thr Asn Gly Phe His Ser Cys Glu Ser Asp Asp Asp Arg Thr
 49 145 150 155 160
 50 Ser His Ala Ser Ser Asp Trp Thr Pro Arg Pro Arg Ile Gly Pro
 51 165 170 175
 52 Tyr Thr Phe Val Gln Gln His Leu Met Ile Gly Thr Asp Pro Arg Thr
 53 180 185 190
 54 Ile Leu Lys Asp Leu Leu Pro Glu Thr Ile Pro Pro Pro Glu Leu Asp

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55          195          200          205
56 Asp Met Thr Leu Trp Gln Ile Val Ile Asn Ile Leu Ser Glu Pro Pro
57          210          215          220
58 Lys Arg Lys Lys Arg Lys Asp Ile Asn Thr Ile Glu Asp Ala Val Lys
59 225          230          235          240
60 Leu Leu Gln Glu Cys Lys Lys Ile Ile Val Leu Thr Gly Ala Gly Val
61          245          250          255
62 Ser Val Ser Cys Gly Ile Pro Asp Phe Arg Ser Arg Asp Gly Ile Tyr
63          260          265          270
64 Ala Arg Leu Ala Val Asp Phe Pro Asp Leu Pro Asp Pro Gln Ala Met
65          275          280          285
66 Phe Asp Ile Glu Tyr Phe Arg Lys Asp Pro Arg Pro Phe Phe Lys Phe
67          290          295          300
68 Ala Lys Glu Ile Tyr Pro Gly Gln Phe Gln Pro Ser Leu Cys His Lys
69 305          310          315          320
70 Phe Ile Ala Leu Ser Asp Lys Glu Gly Lys Leu Leu Arg Asn Tyr Thr
71          325          330          335
72 Gln Asn Ile Asp Thr Leu Glu Gln Val Ala Gly Ile Gln Arg Ile Leu
73          340          345          350
74 Gln Cys His Gly Ser Phe Ala Thr Ala Ser Cys Leu Ile Cys Lys Tyr
75          355          360          365
76 Lys Val Asp Cys Glu Ala Val Arg Gly Asp Ile Phe Asn Gln Val Val
77          370          375          380
78 Pro Arg Cys Pro Arg Cys Pro Ala Asp Glu Pro Leu Ala Ile Met Lys
79 385          390          395          400
80 Pro Glu Ile Val Phe Phe Gly Glu Asn Leu Pro Glu Gln Phe His Arg
81          405          410          415
82 Ala Met Lys Tyr Asp Lys Asp Glu Val Asp Leu Leu Ile Val Ile Gly
83          420          425          430
84 Ser Ser Leu Lys Val Arg Pro Val Ala Leu Ile Pro Ser Ser Ile Pro
85          435          440          445
86 His Glu Val Pro Gln Ile Leu Ile Asn Arg Glu Pro Leu Pro His Leu
87          450          455          460
88 His Phe Asp Val Glu Leu Leu Gly Asp Cys Asp Val Ile Ile Asn Glu
89 465          470          475          480
90 Leu Cys His Arg Leu Gly Gly Glu Tyr Ala Lys Leu Cys Cys Asn Pro
91          485          490          495
92 Val Lys Leu Ser Glu Ile Thr Glu Lys Pro Pro Arg Pro Gln Lys Glu
93          500          505          510
94 Leu Val His Leu Ser Glu Leu Pro Pro Thr Pro Leu His Ile Ser Glu
95          515          520          525
96 Asp Ser Ser Ser Pro Glu Arg Thr Val Pro Gln Asp Ser Ser Val Ile
97          530          535          540
98 Ala Thr Leu Val Asp Gln Ala Thr Asn Asn Asn Val Asn Asp Leu Glu
99 545          550          555          560
100 Val Ser Glu Ser Ser Cys Val Glu Glu Lys Pro Gln Glu Val Gln Thr
101          565          570          575
102 Ser Arg Asn Val Glu Asn Ile Asn Val Glu Asn Pro Asp Phe Lys Ala
103          580          585          590

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```

104 Val Gly Ser Ser Thr Ala Asp Lys Asn Glu Arg Thr Ser Val Ala Glu
105          595          600          605
106 Thr Val Arg Lys Cys Trp Pro Asn Arg Leu Ala Lys Glu Gln Ile Ser
107      610          615          620
108 Lys Arg Leu Glu Gly Asn Gln Tyr Leu Phe Val Pro Pro Asn Arg Tyr
109 625          630          635          640
110 Ile Phe His Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp Asp Val Leu
111          645          650          655
112 Ser Ser Ser Ser Cys Gly Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser
113      660          665          670
114 Pro Ser Leu Glu Glu Pro Leu Glu Asp Glu Ser Glu Ile Glu Glu Phe
115      675          680          685
116 Tyr Asn Gly Leu Glu Asp Asp Thr Glu Arg Pro Glu Cys Ala Gly Gly
117      690          695          700
118 Ser Gly Phe Gly Ala Asp Gly Gly Asp Gln Glu Val Val Asn Glu Ala
119 705          710          715          720
120 Ile Ala Thr Arg Gln Glu Leu Thr Asp Val Asn Tyr Pro Ser Asp Lys
121          725          730          735
122 Ser
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 272
127 <212> TYPE: PRT
128 <213> ORGANISM: Saccharomyces cerevisiae
130 <400> SEQUENCE: 2
131 Ile Asn Lys Val Leu Cys Thr Arg Leu Arg Leu Ser Asn Phe Phe Thr
132 1          5          10          15
133 Ile Asp His Phe Ile Gln Lys Leu His Thr Ala Arg Lys Ile Leu Val
134      20          25          30
135 Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe Arg
136      35          40          45
137 Ser Ser Glu Gly Phe Tyr Ser Lys Ile Lys His Leu Gly Leu Asp Asp
138      50          55          60
139 Pro Gln Asp Val Phe Asn Tyr Asn Ile Phe Met His Asp Pro Ser Val
140 65          70          75          80
141 Phe Tyr Asn Ile Ala Asn Met Val Leu Pro Pro Glu Lys Ile Tyr Ser
142      85          90          95
143 Pro Leu His Ser Phe Ile Lys Met Leu Gln Met Lys Gly Lys Leu Leu
144      100          105          110
145 Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly Ile
146      115          120          125
147 Ser Thr Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala Thr
148      130          135          140
149 Cys Val Thr Cys His Trp Asn Leu Pro Gly Glu Arg Ile Phe Asn Lys
150 145          150          155          160
151 Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Lys Lys Arg
152      165          170          175
153 Arg Glu Tyr Phe Pro Glu Gly Tyr Asn Asn Lys Val Gly Val Ala Ala
154      180          185          190
155 Ser Gln Gly Ser Met Ser Glu Arg Pro Pro Tyr Ile Leu Asn Ser Tyr

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```

156          195          200          205
157 Gly Val Leu Lys Pro Asp Ile Thr Phe Phe Gly Glu Ala Leu Pro Asn
158      210          215          220
159 Lys Phe His Lys Ser Ile Arg Glu Asp Ile Leu Glu Cys Asp Leu Leu
160 225          230          235          240
161 Ile Cys Ile Gly Thr Ser Leu Lys Val Ala Pro Val Ser Glu Ile Val
162          245          250          255
163 Asn Met Val Pro Ser His Val Pro Gln Val Leu Ile Asn Arg Asp Pro
164          260          265          270
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 267
168 <212> TYPE: PRT
169 <213> ORGANISM: Saccharomyces cerevisiae
171 <400> SEQUENCE: 3
172 Ile Asn Lys Val Leu Ser Thr Arg Leu Arg Leu Pro Asn Phe Asn Thr
173 1          5          10          15
174 Ile Asp His Phe Thr Ala Thr Leu Arg Asn Ala Lys Lys Ile Leu Val
175          20          25          30
176 Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe Arg
177          35          40          45
178 Ser Ser Glu Gly Phe Tyr Ser Lys Ile Arg His Leu Gly Leu Glu Asp
179          50          55          60
180 Pro Gln Asp Val Phe Asn Leu Asp Ile Phe Leu Gln Asp Pro Ser Val
181 65          70          75          80
182 Phe Tyr Asn Ile Ala His Met Val Leu Pro Pro Glu Asn Met Tyr Ser
183          85          90          95
184 Pro Leu His Ser Phe Ile Lys Met Leu Gln Asp Lys Gly Lys Leu Leu
185          100          105          110
186 Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly Ile
187          115          120          125
188 Asp Pro Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala Ser
189          130          135          140
190 Cys Val Thr Cys His Trp Gln Ile Pro Gly Glu Lys Ile Phe Glu Asn
191 145          150          155          160
192 Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Gln Lys Arg
193          165          170          175
194 Lys Gln Tyr Phe Pro Met Ser Asn Gly Asn Asn Thr Val Gln Thr Asn
195          180          185          190
196 Ile Asn Phe Asn Ser Pro Ile Leu Lys Ser Tyr Gly Val Leu Lys Pro
197          195          200          205
198 Asp Met Thr Phe Phe Gly Glu Ala Leu Pro Ser Arg Phe His Lys Thr
199          210          215          220
200 Ile Arg Lys Asp Ile Leu Glu Cys Asp Leu Leu Ile Cys Ile Gly Thr
201 225          230          235          240
202 Ser Leu Lys Val Ala Pro Val Ser Glu Ile Val Asn Met Val Pro Ser
203          245          250          255
204 His Val Pro Gln Ile Leu Ile Asn Arg Asp Met
205          260          265
207 <210> SEQ ID NO: 4

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208 <211> LENGTH: 245
209 <212> TYPE: PRT
210 <213> ORGANISM: Mus musculus
212 <400> SEQUENCE: 4
213 Val Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp
214 1 5 10 15
215 Ile Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys
216 20 25 30
217 Ile Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro
218 35 40 45
219 Asp Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe
220 50 55 60
221 Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg
222 65 70 75 80
223 Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly
224 85 90 95
225 Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys
226 100 105 110
227 Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu
228 115 120 125
229 Gln Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His Gly Ser Phe Ala
230 130 135 140
231 Thr Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val
232 145 150 155 160
233 Arg Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro
234 165 170 175
235 Ala Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Phe Gly
236 180 185 190
237 Glu Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp
238 195 200 205
239 Glu Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro
240 210 215 220
241 Val Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu
242 225 230 235 240
243 Ile Asn Arg Glu Pro
244 245
246 <210> SEQ ID NO: 5
247 <211> LENGTH: 237
248 <212> TYPE: PRT
249 <213> ORGANISM: Salmonella typhimurium
251 <400> SEQUENCE: 5
252 Met Met Glu Asn Pro Arg Val Leu Val Leu Thr Gly Ala Gly Ile Ser
253 1 5 10 15
254 Ala Glu Ser Gly Ile Arg Thr Phe Arg Ala Ala Asp Gly Leu Trp Glu
255 20 25 30
256 Glu His Arg Val Glu Asp Val Ala Thr Pro Glu Gly Phe Ala Arg Asn
257 35 40 45
258 Pro Gly Leu Val Gln Thr Phe Tyr Asn Ala Arg Arg Gln Gln Leu Gln
259 50 55 60

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:27; Xaa Pos. 8
Seq#:38; Xaa Pos. 4,6,8